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SEQUENCE LISTING

<110> HER MAJESTY THE QUEEN IN RIGHT OF CANADA, AS REPRESENTED BY THE
MINISTRY OF AGRICULTURE and AGRI-FOOD CANADA

Harris, Linda J.

Gleddie, Stephen C.

<120> TOLERANCE OF TRICHOTHECENE MYCOTOXINS IN PLANTS THROUGH THE
MODIFICATION OF THE RIBOSOMAL PROTEIN L3 GENE

<130> O8-874401US2

<140> US 09/725,957

<141> 2000-11-30

<150> US 09/567,327

<151> 2000-05-09

<150> US 08/909,828

<151> 1997-08-12

<160> 20

<170> PatentIn version 3.0

<210> 1

<211> 350

<212> PRT

<213> Saccharomyces cerevisiae (wild-type)

<400> 1

Met Ser His Arg Lys Tyr Glu Ala Pro Arg His Gly His Leu Gly Phe
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Leu Pro Arg Lys Arg Ala Ala Ser Ile Arg Ala Arg Val Lys Ala Phe
20 25 30

Pro Lys Asp Asp Arg Ser Lys Pro Val Ala Leu Thr Ser Phe Leu Gly
35 40 45

Tyr Lys Ala Gly Met Thr Thr Ile Val Arg Asp Leu Asp Arg Pro Gly
50 55 60

Ser Lys Phe His Lys Arg Glu Val Val Glu Ala Val Thr Val Val Asp
65 70 75 80

Thr Pro Pro Val Val Val Val Gly Val Val Gly Tyr Val Glu Thr Pro
85 90 95

Arg Gly Leu Arg Ser Leu Thr Thr Val Trp Ala Glu His Leu Ser Asp
100 105 110

Glu Val Lys Arg Arg Phe Tyr Lys Asn Trp Tyr Lys Ser Lys Lys Lys
115 120 125

Ala Phe Thr Lys Tyr Ser Ala Lys Tyr Ala Gln Asp Gly Ala Gly Ile
130 135 140

Glu Arg Glu Leu Ala Arg Ile Lys Lys Tyr Ala Ser Val Val Arg Val

145		150		155		160
Leu Val His Thr	Gln Ile Arg Lys Thr	Pro Leu Ala Gln Lys Lys Ala				
	165	170			175	
His Leu Ala Glu Ile Gln Leu Asn Gly Gly Ser Ile Ser Glu Lys Val						
	180	185			190	
Asp Trp Ala Arg Glu His Phe Glu Lys Thr Val Ala Val Asp Ser Val						
	195	200			205	
Phe Glu Gln Asn Glu Met Ile Asp Ala Ile Ala Val Thr Lys Gly His						
	210	215			220	
Gly Phe Glu Gly Val Thr His Arg Trp Gly Thr Lys Lys Leu Pro Arg						
	225	230			235	240
Lys Thr His Arg Gly Leu Arg Lys Val Ala Cys Ile Gly Ala Trp His						
	245	250			255	
Pro Ala His Val Met Trp Ser Val Ala Arg Ala Gly Gln Arg Gly Tyr						
	260	265			270	
His Ser Arg Thr Ser Ile Asn His Lys Ile Tyr Arg Val Gly Lys Gly						
	275	280			285	
Asp Asp Glu Ala Asn Gly Ala Thr Ser Phe Asp Arg Thr Lys Lys Thr						
	290	295			300	
Ile Thr Pro Met Gly Gly Phe Val His Tyr Gly Glu Ile Lys Asn Asp						
	305	310			315	320
Phe Ile Met Val Lys Gly Cys Ile Pro Gly Asn Arg Lys Arg Ile Val						
	325	330			335	
Thr Leu Arg Lys Ser Leu Tyr Thr Asn Thr Ser Arg Lys Ala						
	340	345			350	

<210> 2

<211> 350

<212> PRT

<213> *Saccharomyces cerevisiae* (trichodermin-resistant)

<400> 2

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	20			25				30	
Pro Lys Asp Asp Arg Ser Lys Pro Val Ala Leu Thr Ser Phe Leu Gly									
	35			40				45	
Tyr Lys Ala Gly Met Thr Thr Ile Val Arg Asp Leu Asp Arg Pro Gly									
	50			55				60	
Ser Lys Phe His Lys Arg Glu Val Val Glu Ala Val Thr Val Val Asp									
	65			70				75	80

Thr Pro Pro Val Val Val Val Gly Val Val Gly Tyr Val Glu Thr Pro
85 90 95

Arg Gly Leu Arg Ser Leu Thr Thr Val Trp Ala Glu His Leu Ser Asp
100 105 110

Glu Val Lys Arg Arg Phe Tyr Lys Asn Trp Tyr Lys Ser Lys Lys Lys
115 120 125

Ala Phe Thr Lys Tyr Ser Ala Lys Tyr Ala Gln Asp Gly Ala Gly Ile
130 135 140

Glu Arg Glu Leu Ala Arg Ile Lys Lys Tyr Ala Ser Val Val Arg Val
145 150 155 160

Leu Val His Thr Gln Ile Arg Lys Thr Pro Leu Ala Gln Lys Lys Ala
165 170 175

His Leu Ala Glu Ile Gln Leu Asn Gly Gly Ser Ile Ser Glu Lys Val
180 185 190

Asp Trp Ala Arg Glu His Phe Glu Lys Thr Val Ala Val Asp Ser Val
195 200 205

Phe Glu Gln Asn Glu Met Ile Asp Ala Ile Ala Val Thr Lys Gly His
210 215 220

Gly Phe Glu Gly Val Thr His Arg Trp Gly Thr Lys Lys Leu Pro Arg
225 230 235 240

Lys Thr His Arg Gly Leu Arg Lys Val Ala Cys Ile Gly Ala Cys His
245 250 255

Pro Ala His Val Met Trp Ser Val Ala Arg Ala Gly Gln Arg Gly Tyr
260 265 270

His Ser Arg Thr Ser Ile Asn His Lys Ile Tyr Arg Val Gly Lys Gly
275 280 285

Asp Asp Glu Ala Asn Gly Ala Thr Ser Phe Asp Arg Thr Lys Lys Thr
290 295 300

Ile Thr Pro Met Gly Gly Phe Val His Tyr Gly Glu Ile Lys Asn Asp
305 310 315 320

Phe Ile Met Val Lys Gly Cys Ile Pro Gly Asn Arg Lys Arg Ile Val
325 330 335

Thr Leu Arg Lys Ser Leu Tyr Thr Asn Thr Ser Arg Lys Ala
340 345 350

<210> 3

<211> 389

<212> PRT

<213> Orzya sativa

<400> 3

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 20 25 30
 Pro Lys Asp Asp Val Ser Lys Pro Cys His Leu Thr Ser Phe Val Gly
 35 40 45
 Tyr Lys Ala Gly Met Thr His Ile Val Arg Glu Val Glu Lys Pro Gly
 50 55 60
 Ser Lys Leu His Lys Lys Glu Thr Cys Glu Ala Val Thr Ile Ile Glu
 65 70 75 80
 Thr Pro Pro Leu Val Ile Val Gly Leu Val Ala Tyr Val Lys Thr Pro
 85 90 95
 Arg Gly Leu Arg Ser Leu Asn Ser Val Trp Ala Gln His Leu Ser Glu
 100 105 110
 Glu Val Arg Arg Arg Phe Tyr Lys Asn Trp Cys Lys Ser Lys Lys Lys
 115 120 125
 Ala Phe Thr Lys Tyr Ala Leu Lys Tyr Asp Ser Asp Ala Gly Lys Lys
 130 135 140
 Glu Ile Gln Met Gln Leu Glu Lys Met Lys Lys Tyr Ala Ser Ile Val
 145 150 155 160
 Arg Val Ile Ala His Thr Gln Ile Arg Lys Met Lys Gly Leu Lys Gln
 165 170 175
 Lys Lys Ala His Leu Met Glu Ile Gln Ile Asn Gly Gly Thr Ile Ala
 180 185 190
 Asp Lys Val Asp Tyr Gly Tyr Lys Phe Phe Glu Lys Glu Ile Pro Val
 195 200 205
 Asp Ala Val Phe Gln Lys Asp Glu Met Ile Asp Ile Ile Gly Val Thr
 210 215 220
 Lys Gly Lys Gly Tyr Glu Gly Val Val Thr Arg Trp Gly Val Thr Arg
 225 230 235 240
 Leu Pro Arg Lys Thr His Arg Gly Leu Arg Lys Val Ala Cys Ile Gly
 245 250 255
 Ala Trp His Pro Ala Arg Val Ser Tyr Thr Val Ala Arg Ala Gly Gln
 260 265 270
 Asn Gly Tyr His His Arg Thr Glu Met Asn Lys Lys Val Tyr Lys Ile
 275 280 285
 Gly Lys Ser Gly Gln Glu Ser His Ala Ala Cys Thr Glu Phe Asp Arg
 290 295 300
 Thr Glu Lys Asp Ile Thr Pro Met Gly Gly Phe Pro His Tyr Gly Val
 305 310 315 320
 Val Lys Gly Asp Tyr Leu Met Ile Lys Gly Cys Cys Val Gly Pro Lys
 325 330 335
 Lys Arg Val Val Thr Leu Arg Gln Ser Leu Leu Lys Gln Thr Ser Arg
 340 345 350
 Leu Ala Leu Glu Glu Ile Lys Leu Lys Phe Ile Asp Thr Ser Ser Lys
 355 360 365

Phe Gly His Gly Arg Phe Gln Thr Thr Asp Glu Lys Gln Arg Phe Phe
370 375 380

Gly Lys Leu Lys Ala
385

<210> 4

<211> 18

<212> DNA

<213> Artificial

<220>

<223> Oligomer

<400> 4

ggctggatgg caggcacc

18

<210> 5

<211> 18

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 5

aagcgaccgt gcccgaaac

18

<210> 6

<211> 18

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 6

gtcgcacagg aagttcga

18

<210> 7

<211> 1281

<212> DNA

<213> Zea mays

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tgccatctca ctgccttctt tggctacaag gctggcatga ctcacattgt ccgtgaggtt 180
gagaagccag gatccaaact ccataagaag gaaacttggt aggctgttac catcattgaa 240
acccctcttc ttgtcattgt tgggtcgtg gcataatgta agactcctcg tggcctccgc 300
acacccaact ctgtttgggc ccaacatctt agcgaagaag tgaggagaag gttctacaag 360
aactggtgca agagcaagaa gaaggctttc acaaagtatg ctctcaaata tgaaaatgat 420
gctggcaaga aggaaattca gctgcagctt gagaagatga agaaatatgc ttctgtttatc 480
cgtgtcattg ctcataccca gattaggaag atgaagggtt tgaagcagaa gaaggctcac 540
ctgatggaga ttcaggtcaa tgggtgtacc attgctgaca aggtggacta tggctacaaa 600
ttttttgaga aagaggtccc tgttgatgct gtcttccaga aggatgagat gattgacatc 660
attggtgtga ccaaaggtaa aggttatgag ggtgtggtca ctcgttgggg tgtcacccgc 720
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gctagggctt cctatacggg tggcgtgct ggtcagaatg ggtaccacca ccgcaactgag 840
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gagtttgaca ggaccgagaa ggacatcact cccatgggtg gcttccccca ctatggtatc 960
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aaaatcatca aactgtgata cttttgtttg taaccttgc gtaccaagtt ttgtagccgg 1260
atgggttcggg cacggctcgt t 1281

<210> 8

<211> 1282

<212> DNA

<213> Zea mays

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cgctcctccc gtcaccgcgg caaggtgaag tcattccta gggatgaccc caagaagcct 120
tgccatctca ctgccttctt tggctacaag gctggcatga ctcacattgt ccgtgaggtt 180

gagaagccag gatccaaact ccataagaag gaaacttggtg aggctgttac catcattgaa	240
acccctcctc ttgtcattgt tgggctcgtg gcatatgtga agactccccg tggcctccgc	300
acactcaact ctgtttgggc ccaacatott agcgaagaag tgaggagaag gttctacaag	360
aactgggtgca agagcaagaa gaaggctttc acaaagtatg ctctcaaata tgaaaatgat	420
gctggcaaga aggaaattca gctgcagctt gagaagatga agaaatatgc ttctgttatac	480
cgtgtcattg ctcataccca gattaggaag atgaagggtt tgaagcagaa gaaggctcac	540
ctgatggaga ttcaggtcaa tgggtgtacc attgctgaca aggtggacta tggctacaaa	600
ttctttgaga aagaggtccc tgttgatgct gtcttccaga aggatgagat gattgacatc	660
attgggtgtga ccaaggggaa aggttatgag ggtgtgggtca ctcgttgggg tgtcacccgg	720
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gagtttgaca ggactgagaa ggacatcact cccatgggtg gcttccccca ttatggtatc	960
gtgaagggtg actacctgat gatcaagggc tgctgtgtgg gtccaaagaa gaggggtggtg	1020
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aagttcatcg acacatcgtc caagttcggg cacggctcgt tccagactac cgatgagaag	1140
cagaggttct ttggcaagct caaggcgtaa ggtgctgcgg tgcagcgaag tcccatttct	1200
caaaatcatc aaactgtgat acttttgttt gtaaccttgc tgtaccaagt tttgtagccg	1260
gatggttcgg gcacggtcgc tt	1282

<210> 9

<211> 1144

<212> DNA

<213> Avena sativa

<400> 9

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cgtactctta acactgtctg ggctcagcat ctcagtgaag acgttaggag gaggttctac	180
aagaactggt gcaagagcaa gaagaaggct ttcaccaagt atgctctcaa gtatgacagt	240
gatgcaggca agaaggaaat tcagctgcag cttgagaaga tgaagaagta tggcactgtt	300
atccgagtta tcgccatac ccagataagg aagatgaagg gcttgaagca gaagaaggct	360
cacctgatgg agatccaggt caatggtggc accatcgag acaagggtgga ctatggctac	420
aatttctttg agaaggaagt cccattgat gctgtcttcc agaaggatga gatgattgac	480

atcatcggtg	tcaccaaggg	taagggatac	gaggggtgtg	tgacacggtg	gggtgtcacc	540
cgcttcccc	gcaagacca	cagaggtctc	cgcaagggtg	cctgcattgg	tgcttggcat	600
ccggctaggg	tttctacac	tggtgcccgt	gctgggtcaga	atggatacca	ccaccgaact	660
gagatgaaca	agaagattta	caagatcggc	aagggttgac	aggaaactca	tgatgcctcc	720
acagagttcg	acaggactga	gaaggacatc	acccccatgg	gtggcttccc	ccactacggt	780
gtggtgaagg	gtgactacct	catgatcaag	ggatgctgcg	ttggcccgaa	gaagcgtgtg	840
gtgaccctcc	gccagtcctt	gctgaagcag	acctcccgtc	tggccctgga	ggagatcaag	900
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aagcagaggt	tctatggcaa	gctcaaggcc	tgaactgctg	gaccgctgca	tcagttatat	1020
cattttgtca	aaacgaatat	ctgatacttg	gttcctttcc	ttgcccctaa	gttttgtagc	1080
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aaaa						1144

<210> 10

<211> 1319

<212> DNA

<213> Hordeum vulgare

<400> 10

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tgccacctca	ctgccttctt	tggttacaag	gctggcatga	ctcacattgt	gcgtgaggtc	180
gagaagcctg	gttccaagct	gcacaagaag	gagacatgtg	aggctgtcac	cattgttgag	240
acacccccta	ttgttattgt	tggaactgtt	gcctatgtga	agactcctcg	tggccttcgt	300
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aactggtgca	agagcaagaa	gaaggccttc	accaagtatg	cgctgaagta	tgacagtgat	420
gctggcaaga	aagaaatcca	gatgcagctt	gagaagatga	agaagtatgc	tactgttgct	480
cgtgttattg	cccatacca	gatcaggaag	atgaaggggc	tgaagcagaa	gaaggctcac	540
ctcatggaga	tccagatcaa	tggtggcacc	attgccgata	aggtggacta	tggttacaac	600
ttctttgaga	aggaagtccc	cattgatgcg	gttttccaaa	argatgagat	gattgatatc	660
attggtgtaa	ccaagggtaa	gggttatgaa	ggtgttgtga	cacgttgggg	tgacacccgc	720
cttccccgca	agaccacag	aggctcttcg	aagggtgcct	gtattggtgc	ctggcatcct	780
gctagggtgt	cctacactgt	tgctcgggct	ggtcagaatg	gataccacca	ccggactgag	840
atgaacaaga	aggtgtacaa	gattggcaag	gttggmcagg	aaacccatga	tgctctact	900

gagttcgaca ggaccgagaa ggacatcact cccatgggtg gcttccctca ctatgggtgtg	960
gtgaaggccg actacctgat gatcaagga tgctgtgtcg ggccaaagaa gcgtgtggtg	1020
accctccgcc agtccctgct gaagcagacc tctcgtctcg cactygagga aatcaagctc	1080
aagttggkcg acacctcttt caagtttggg cacgggcccgt ttcaagacac ggacgagaag	1140
cagaggttct ttggcaagct caaggctgag ctgctgggca tatagttggg tcttttgtsa	1200
aacgaacttg gaaaccttgt tactttcctg gcctaagttt gagctgggggt gdcamgaatc	1260
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<210> 11

<211> 587

<212> DNA

<213> Sorghum vulgare

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tgccacctca ccgccttcct tggctacaag gctggcayga ctcacattgt gcgtgaggtc	180
gagaagcctg gatccaaact acacaagaag gaaacgtgtg aggctgttac catcattgaa	240
accctcctc tggtcattgt tgggcttgtg gcatatgtga agactsctcg cggcctccgc	300
acactcaaca ctgtttgggc tcagcatctt agcgaagaag ttaggagaag gttctacaag	360
aactggtgca agagcaagaa gaaggctttc tccaagtatg ctctcaagta tgacaatgat	420
gctggcaaga aggaaattca gctgcagctt gagaagatga agaaatatgc ttctgttgtc	480
cgtgtcattg cccataccca gattaagaag atgaagggtt tgaagcagaa gaaggctcat	540
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<210> 12

<211> 1330

<212> DNA

<213> Sorghum vulgare

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tgccacctca ccgcatttgt tggctacaag gctggaatga cacacattgt gcgtgaggtg	180
gagaagcctg gctccaagct ccacaagaag gaaacttgtg aggctgtgac tatcattgag	240

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aactgggtgca	agagcaagaa	gaaggccttc	accaagtaag	ccctcaaata	tgacagcgac	420
gcaggcaaga	aagaaatcca	gttgcagctt	gagaagatga	agaagtatgc	ttcagttatc	480
cgtgttatcg	cccacactca	gattaaaaag	atgaaagggt	tgaagcagaa	gaaggctcac	540
cttatggaga	tccagggtcaa	tggtggcact	atagcagaca	aggtggacta	tggttacaaa	600
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attggagtca	ccaagggtaa	ggggtatgaa	ggtgtggtca	ctcgttgggg	tgttaccggg	720
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gagtttgaca	ggactgagaa	ggacatcact	cccatgggtg	gcttccccca	ctatggtatt	960
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ggaattgtat	tacctgatag	tattttgttt	ttcttcagtt	ttgttgagaa	tatcagaaga	1260
acatgtttga	ttttctagtc	tgagctactt	ccattgcgga	tgattgatat	tgatattatt	1320
gcaaattctg						1330

<210> 13

<211> 1344

<212> DNA

<213> *Triticum aestivum*

<400> 13

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gagaagcctg	gttccaagct	acacaagaag	gagacatgtg	aggctgtcac	cattgttgag	240
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aactgggtgca	agagcaagaa	gaaggccttc	accaagtatg	ctctgaagta	tgacagtgat	420
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<210> 14

<211> 389

<212> PRT

<213> Zea mays

<400> 14

Met Ser His Arg Lys Phe Glu His Pro Arg His Gly Ser Leu Gly Phe
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20 25 30
Pro Arg Asp Asp Pro Lys Lys Pro Cys His Leu Thr Ala Phe Leu Gly
35 40 45
Tyr Lys Ala Gly Met Thr His Ile Val Arg Glu Val Glu Lys Pro Gly
50 55 60
Ser Lys Leu His Lys Lys Glu Thr Cys Glu Ala Val Thr Ile Ile Glu
65 70 75 80
Thr Pro Pro Leu Val Ile Val Gly Leu Val Ala Tyr Val Lys Thr Pro
85 90 95
Arg Gly Leu Arg Thr Leu Asn Ser Val Trp Ala Gln His Leu Ser Glu
100 105 110
Glu Val Arg Arg Arg Phe Tyr Lys Asn Trp Cys Lys Ser Lys Lys Lys

115					120					125					
Ala	Phe	Thr	Lys	Tyr	Ala	Leu	Lys	Tyr	Glu	Asn	Asp	Ala	Gly	Lys	Lys
130					135					140					
Glu	Ile	Gln	Leu	Gln	Leu	Glu	Lys	Met	Lys	Lys	Tyr	Ala	Ser	Val	Ile
145					150					155					160
Arg	Val	Ile	Ala	His	Thr	Gln	Ile	Arg	Lys	Met	Lys	Gly	Leu	Lys	Gln
				165					170					175	
Lys	Lys	Ala	His	Leu	Met	Glu	Ile	Gln	Val	Asn	Gly	Gly	Thr	Ile	Ala
			180					185					190		
Asp	Lys	Val	Asp	Tyr	Gly	Tyr	Lys	Phe	Phe	Glu	Lys	Glu	Val	Pro	Val
		195					200					205			
Asp	Ala	Val	Phe	Gln	Lys	Asp	Glu	Met	Ile	Asp	Ile	Ile	Gly	Val	Thr
	210					215					220				
Lys	Gly	Lys	Gly	Tyr	Glu	Gly	Val	Val	Thr	Arg	Trp	Gly	Val	Thr	Arg
225					230					235					240
Leu	Pro	Arg	Lys	Thr	His	Arg	Gly	Leu	Arg	Lys	Val	Ala	Cys	Ile	Gly
				245					250					255	
Ala	Trp	His	Pro	Ala	Arg	Val	Ser	Tyr	Thr	Val	Ala	Arg	Ala	Gly	Gln
			260					265					270		
Asn	Gly	Tyr	His	His	Arg	Thr	Glu	Met	Asn	Lys	Lys	Val	Tyr	Lys	Ile
		275					280					285			
Gly	Lys	Ala	Gly	Gln	Glu	Thr	His	Asp	Ala	Ser	Thr	Glu	Phe	Asp	Arg
	290					295					300				
Thr	Glu	Lys	Asp	Ile	Thr	Pro	Met	Gly	Gly	Phe	Pro	His	Tyr	Gly	Ile
305					310					315					320
Val	Lys	Gly	Asp	Tyr	Leu	Met	Ile	Lys	Gly	Cys	Cys	Val	Gly	Pro	Lys
				325					330					335	
Lys	Arg	Val	Val	Thr	Leu	Arg	Gln	Ser	Leu	Leu	Lys	Gln	Thr	Ser	Arg
			340					345					350		
Leu	Ala	Leu	Glu	Glu	Ile	Lys	Leu	Lys	Phe	Ile	Asp	Thr	Ser	Ser	Lys
	355						360				365				
Phe	Gly	His	Gly	Arg	Phe	Gln	Thr	Thr	Asp	Glu	Lys	Gln	Arg	Phe	Phe
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Gly Lys Leu Lys Ala
385

<210> 15

<211> 389

<212> PRT

<213> Sorghum vulgare

<400> 15

Met	Ser	His	Arg	Lys	Phe	Glu	His	Pro	Arg	His	Gly	Ser	Leu	Ser	Phe	1	5	10	15
Leu	Pro	Asn	Lys	Arg	Ser	Ser	Arg	His	Arg	Gly	Lys	Val	Lys	Ser	Phe	20	25	30	
Pro	Arg	Asp	Asp	Pro	Lys	Lys	Pro	Cys	His	Leu	Thr	Ala	Phe	Val	Gly	35	40	45	
Tyr	Lys	Ala	Gly	Met	Thr	His	Ile	Val	Arg	Glu	Val	Glu	Lys	Pro	Gly	50	55	60	
Ser	Lys	Leu	His	Lys	Lys	Glu	Thr	Cys	Glu	Ala	Val	Thr	Ile	Ile	Glu	65	70	75	80
Thr	Pro	Pro	Leu	Val	Ile	Val	Gly	Leu	Val	Ala	Tyr	Val	Lys	Thr	Pro	85	90	95	
Arg	Gly	Leu	Arg	Thr	Leu	Asn	Ser	Val	Trp	Ala	Gln	His	Leu	Ser	Glu	100	105	110	
Glu	Val	Arg	Arg	Arg	Phe	Tyr	Lys	Asn	Trp	Cys	Lys	Ser	Lys	Lys	Lys	115	120	125	
Ala	Phe	Thr	Lys	Tyr	Ala	Leu	Lys	Tyr	Asp	Ser	Asp	Ala	Gly	Lys	Lys	130	135	140	
Glu	Ile	Gln	Leu	Gln	Leu	Glu	Lys	Met	Lys	Lys	Tyr	Ala	Ser	Val	Ile	145	150	155	160
Arg	Val	Ile	Ala	His	Thr	Gln	Ile	Lys	Lys	Met	Lys	Gly	Leu	Lys	Gln	165	170	175	
Lys	Lys	Ala	His	Leu	Met	Glu	Ile	Gln	Val	Asn	Gly	Gly	Thr	Ile	Ala	180	185	190	
Asp	Lys	Val	Asp	Tyr	Gly	Tyr	Lys	Phe	Phe	Glu	Lys	Glu	Val	Pro	Val	195	200	205	
Asp	Ala	Val	Phe	Gln	Lys	Asp	Glu	Met	Ile	Asp	Ile	Ile	Gly	Val	Thr	210	215	220	
Lys	Gly	Lys	Gly	Tyr	Glu	Gly	Val	Val	Thr	Arg	Trp	Gly	Val	Thr	Arg	225	230	235	240
Leu	Pro	Arg	Lys	Thr	His	Arg	Gly	Leu	Arg	Lys	Val	Ala	Cys	Ile	Gly	245	250	255	
Ala	Trp	His	Pro	Ala	Arg	Val	Ser	Tyr	Thr	Val	Ala	Arg	Ala	Gly	Gln	260	265	270	
Asn	Gly	Tyr	His	His	Arg	Thr	Glu	Met	Asn	Lys	Lys	Val	Tyr	Lys	Ile	275	280	285	
Gly	Lys	Ala	Gly	Gln	Glu	Ser	His	Asp	Ala	Ser	Thr	Glu	Phe	Asp	Arg	290	295	300	
Thr	Glu	Lys	Asp	Ile	Thr	Pro	Met	Gly	Gly	Phe	Pro	His	Tyr	Gly	Ile	305	310	315	320
Val	Lys	Gly	Asp	Tyr	Leu	Met	Ile	Lys	Gly	Cys	Cys	Val	Gly	Pro	Lys	325	330	335	
Lys	Arg	Val	Val	Thr	Leu	Arg	Gln	Ser	Leu	Leu	Lys	Gln	Thr	Ser	Arg	340	345	350	

Leu Ala Leu Glu Glu Ile Lys Leu Lys Phe Ile Asp Thr Ser Ser Lys
355 360 365

Phe Gly His Gly Arg Phe Gln Thr Thr Asp Glu Lys Gln Lys Phe Tyr
370 375 380

Gly Lys Gln Lys Ala
385

<210> 16

<211> 389

<212> PRT

<213> Triticum aestivum

<400> 16

Met Ser His Arg Lys Phe Glu His Pro Arg His Gly Ser Leu Gly Phe
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Leu Pro Arg Lys Arg Cys Ser Arg His Arg Gly Lys Val Lys Ala Phe
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Pro Arg Asp Asp Gln Ser Lys Lys Cys His Leu Thr Ala Phe Leu Gly
35 40 45

Tyr Lys Ala Gly Met Thr His Ile Val Arg Glu Val Glu Lys Pro Gly
50 55 60

Ser Lys Leu His Lys Lys Glu Thr Cys Glu Ala Val Thr Ile Val Glu
65 70 75 80

Thr Pro Pro Ile Val Ile Val Gly Leu Val Ala Tyr Val Lys Thr Pro
85 90 95

Arg Gly Leu Arg Thr Leu Asn Ser Val Trp Ala Gln His Leu Ser Glu
100 105 110

Asp Val Arg Arg Arg Phe Tyr Lys Asn Trp Cys Lys Ser Lys Lys Lys
115 120 125

Ala Phe Thr Lys Tyr Ala Leu Lys Tyr Asp Ser Asp Ala Gly Lys Lys
130 135 140

Glu Ile Gln Met Gln Leu Glu Lys Met Lys Lys Tyr Ala Thr Val Val
145 150 155 160

Arg Val Ile Ala His Thr Gln Ile Arg Lys Met Lys Gly Leu Lys Gln
165 170 175

Lys Lys Ala His Leu Met Glu Ile Gln Ile Asn Gly Gly Thr Ile Ala
180 185 190

Asp Lys Val Asp Tyr Gly Tyr Asn Phe Phe Glu Lys Glu Val Pro Ile
195 200 205

Asp Ala Val Phe Gln Lys Asp Glu Met Ile Asp Ile Ile Gly Val Thr
210 215 220

Lys Gly Lys Gly Tyr Glu Gly Val Val Thr Arg Trp Gly Val Thr Arg
225 230 235 240

Leu Pro Arg Lys Thr His Arg Gly Leu Arg Lys Val Ala Cys Ile Gly
245 250 255

Ala Trp His Pro Ala Arg Val Ser Tyr Thr Val Ala Arg Ala Gly Gln
260 265 270

Asn Gly Tyr His His Arg Thr Glu Met Asn Lys Lys Val Tyr Lys Ile
275 280 285

Gly Lys Val Gly Gln Glu Thr His Asp Ala Ser Thr Glu Phe Asp Arg
290 295 300

Thr Glu Lys Asp Ile Thr Pro Met Gly Gly Phe Pro His Tyr Gly Val
305 310 315 320

Val Lys Ala Asp Tyr Leu Met Ile Lys Gly Cys Cys Val Gly Pro Lys
325 330 335

Lys Arg Val Val Thr Leu Arg Gln Ser Leu Leu Lys Gln Thr Ser Arg
340 345 350

Leu Ala Leu Glu Glu Ile Lys Leu Lys Phe Val Asp Thr Ser Ser Lys
355 360 365

Phe Gly His Gly Arg Phe Gln Thr Thr Asp Glu Lys Gln Arg Phe Tyr
370 375 380

Gly Lys Leu Lys Ala
385

<210> 17

<211> 389

<212> PRT

<213> Hordeum vulgare

<220>

<221> misc_feature

<223> Xaa="ANY AMINO ACID SEQUENCE"

<400> 17

Met Ser His Arg Lys Phe Glu His Pro Arg His Gly Ser Leu Gly Phe
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Pro Arg Asp Asp Gln Ser Lys Lys Cys His Leu Thr Ala Phe Leu Gly
35 40 45

Tyr Lys Ala Gly Met Thr His Ile Val Arg Glu Val Glu Lys Pro Gly
50 55 60

Ser Lys Leu His Lys Lys Glu Thr Cys Glu Ala Val Thr Ile Val Glu
65 70 75 80

Thr Pro Pro Ile Val Ile Val Gly Leu Val Ala Tyr Val Lys Thr Pro
85 90 95

Arg Gly Leu Arg Thr Leu Asn Ser Val Trp Ala Gln His Leu Ser Glu
100 105 110

Asp Val Arg Arg Arg Phe Tyr Lys Asn Trp Cys Lys Ser Lys Lys Lys
115 120 125

Ala Phe Thr Lys Tyr Ala Leu Lys Tyr Asp Ser Asp Ala Gly Lys Lys
130 135 140

Glu Ile Gln Met Gln Leu Glu Lys Met Lys Lys Tyr Ala Thr Val Val
145 150 155 160

Arg Val Ile Ala His Thr Gln Ile Arg Lys Met Lys Gly Leu Lys Gln
165 170 175

Lys Lys Ala His Leu Met Glu Ile Gln Ile Asn Gly Gly Thr Ile Ala
180 185 190

Asp Lys Val Asp Tyr Gly Tyr Asn Phe Phe Glu Lys Glu Val Pro Ile
195 200 205

Asp Ala Val Phe Gln Lys Asp Glu Met Ile Asp Ile Ile Gly Val Thr
210 215 220

Lys Gly Lys Gly Tyr Glu Gly Val Val Thr Arg Trp Gly Val Thr Arg
225 230 235 240

Leu Pro Arg Lys Thr His Arg Gly Leu Arg Lys Val Ala Cys Ile Gly
245 250 255

Ala Trp His Pro Ala Arg Val Ser Tyr Thr Val Ala Arg Ala Gly Gln
260 265 270

Asn Gly Tyr His His Arg Thr Glu Met Asn Lys Lys Val Tyr Lys Ile
275 280 285

Gly Lys Val Gly Gln Glu Thr His Asp Ala Ser Thr Glu Phe Asp Arg
290 295 300

Thr Glu Lys Asp Ile Thr Pro Met Gly Gly Phe Pro His Tyr Gly Val
305 310 315 320

Val Lys Ala Asp Tyr Leu Met Ile Lys Gly Cys Cys Val Gly Pro Lys
325 330 335

Lys Arg Val Val Thr Leu Arg Gln Ser Leu Leu Lys Gln Thr Ser Arg
340 345 350

Leu Ala Leu Glu Glu Ile Lys Leu Lys Leu Xaa Asp Thr Ser Phe Lys
355 360 365

Phe Gly His Gly Pro Phe Gln Asp Thr Asp Glu Lys Gln Arg Phe Phe
370 375 380

Gly Lys Leu Lys Ala
385

<210> 18

<211> 330

<212> PRT

<213> Avena sativa

<400> 18

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Tyr	Val	Lys	Thr	Pro	Arg	Gly	Leu	Arg	Thr	Leu	Asn	Thr	Val	Trp	Ala	35	40	45	
Gln	His	Leu	Ser	Glu	Asp	Val	Arg	Arg	Arg	Phe	Tyr	Lys	Asn	Trp	Cys	50	55	60	
Lys	Ser	Lys	Lys	Lys	Ala	Phe	Thr	Lys	Tyr	Ala	Leu	Lys	Tyr	Asp	Ser	65	70	75	80
Asp	Ala	Gly	Lys	Lys	Glu	Ile	Gln	Leu	Gln	Leu	Glu	Lys	Met	Lys	Lys	85	90	95	
Tyr	Gly	Thr	Val	Ile	Arg	Val	Ile	Ala	His	Thr	Gln	Ile	Arg	Lys	Met	100	105	110	
Lys	Gly	Leu	Lys	Gln	Lys	Lys	Ala	His	Leu	Met	Glu	Ile	Gln	Val	Asn	115	120	125	
Gly	Gly	Thr	Ile	Ala	Asp	Lys	Val	Asp	Tyr	Gly	Tyr	Asn	Phe	Phe	Glu	130	135	140	
Lys	Glu	Val	Pro	Ile	Asp	Ala	Val	Phe	Gln	Lys	Asp	Glu	Met	Ile	Asp	145	150	155	160
Ile	Ile	Gly	Val	Thr	Lys	Gly	Lys	Gly	Tyr	Glu	Gly	Val	Val	Thr	Arg	165	170	175	
Trp	Gly	Val	Thr	Arg	Leu	Pro	Arg	Lys	Thr	His	Arg	Gly	Leu	Arg	Lys	180	185	190	
Val	Ala	Cys	Ile	Gly	Ala	Trp	His	Pro	Ala	Arg	Val	Ser	Tyr	Thr	Val	195	200	205	
Ala	Arg	Ala	Gly	Gln	Asn	Gly	Tyr	His	His	Arg	Thr	Glu	Met	Asn	Lys	210	215	220	
Lys	Ile	Tyr	Lys	Ile	Gly	Lys	Val	Gly	Gln	Glu	Thr	His	Asp	Ala	Ser	225	230	235	240
Thr	Glu	Phe	Asp	Arg	Thr	Glu	Lys	Asp	Ile	Thr	Pro	Met	Gly	Gly	Phe	245	250	255	
Pro	His	Tyr	Gly	Val	Val	Lys	Gly	Asp	Tyr	Leu	Met	Ile	Lys	Gly	Cys	260	265	270	
Cys	Val	Gly	Pro	Lys	Lys	Arg	Val	Val	Thr	Leu	Arg	Gln	Ser	Leu	Leu	275	280	285	
Lys	Gln	Thr	Ser	Arg	Leu	Ala	Leu	Glu	Glu	Ile	Lys	Leu	Lys	Phe	Val	290	295	300	
Asp	Thr	Ser	Ser	Lys	Phe	Gly	His	Gly	Arg	Phe	Gln	Thr	Thr	Asp	Glu	305	310	315	320

Lys Gln Arg Phe Tyr Gly Lys Leu Lys Ala
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<210> 19

<211> 1347

<212> DNA

<213> Orzya sativa

<400> 19

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<210> 20

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<212> DNA

<213> Artifical

<220>

<223> Consensus

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